

GenCore version 5.1.7  
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 AWM protein - protein search, using sw model  
 Run on: March 2, 2006, 04:10:57 ; Search time 185 Seconds  
 (without alignments)  
 121.126 Million cell updates/sec  
 Title: US-10-077-438-1\_COPY\_1\_51  
 Perfect score: 51  
 Sequence: MLCMAGQCSQNBYFDSLHAA.....TPPLTCQRCNASVTNSVKG 51  
 Scoring table: OBEGO  
 Gappen: 60.0 , Gapext 60.0  
 Searched: 2443163 seqs, 439378781 residues  
 Aae00507 Human BCM  
 Adg13717 Human B-C  
 Aae15485 Human B-C  
 Aae15484 Human B-C  
 Abr01082 Human GEN  
 Aae15488 Human BCM  
 Abg9060 Human tra  
 Aae15501 Human B-C  
 Adz67761 Human tum  
 Aec02033 Amino aci  
 Aae15486 Human B-C  
 Ada43366 Human BCM  
 Aec02042 Amino aci  
 Aec02026 Formula I  
 Aec02024 Formula I  
 Abj38417 TALL-1 re  
 Adi53060 Human BCM  
 Aec02020 Formula I  
 Aec02028 Formula I  
 Aec02017 Formula I

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

**Post-processing:** Listing first 45 summaries

卷之三

1: geneseqp1980s:\*

\* १२३ देवदत्त शुभार्थी २५८

```
4: geneseq2001s:*
```

geneseqp2003as:\*

Digitized by srujanika@gmail.com

9: generaetp20058: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES						
result	No.	Query Score	Match Length	DB ID	Description	
1	1	51	100.0	52	9	AEC0032 Amino aci
	2	51	100.0	184	3	AAB0843 Amino aci
	3	51	100.0	184	3	AAY94001 A human B
	4	51	100.0	184	4	AAB0241 Human BCM
	5	51	100.0	184	4	AAY71979 Human B C
	6	51	100.0	184	4	Aab0698 Human BAF
	7	51	100.0	184	4	Aae00506 Human B C
	8	51	100.0	184	5	ABBB487 Human BCM
	9	51	100.0	184	5	ABP5694 Metastaci
	10	51	100.0	184	5	Aae29961 Human B-C
	11	51	100.0	184	6	Aae32116 Human B-C
	12	51	100.0	184	6	ADA43361 Human Bum
	13	51	100.0	184	6	ABP6552 Human Bum
	14	51	100.0	184	6	ABP9717 Amino aci
	15	51	100.0	184	7	ADD67527 Human Ly1
	16	51	100.0	184	7	ADG43715 Human B-C
	17	51	100.0	184	8	Adk00756 Human hu
	18	51	100.0	184	8	Adq9442 Neutrokin
	19	51	100.0	184	8	Adp5614 Human PRO
	20	51	100.0	184	9	ADW0432 Human BCM
	21	51	100.0	184	9	ADZ67760 Human tum
	22	51	100.0	184	9	Aea23348 Tumor ant
	23	51	100.0	184	9	Aec0031 Amino acid
	24	51	100.0	184	9	Abd05699 Mouse Trc

ALIGNMENT S.

RESULT 1	
AEC02032	ABC02032 standard; peptide; 52 AA.
ID	ABC02032
XX	XX
AC	AECC02032;
XX	DT
XX	20-OCT-2005 (first entry)
DE	Amino acid sequence of an extracellular dom
XX	APRIL; Baff; immune disorder; immunomodulatory
KW	cytokine; neoplasm; immunosuppressive; th
R-cell maturation antigen; BCMA	R-cell
KW	
KW	

**Synthetic.**  
WO2005075511-A1.  
18-AUG-2005.  
04-AUG-2004; 2004WO-US025247.  
29-JAN-2004; 2004US-0540271P.  
(GETH ) GENENTECH INC.  
Kellley RF, Patel D;  
WPI; 2005-555932/56.  
New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
for treating immune related disease, cancer or T-cell mediated disease

such as graft rejection, graft-versus-host disease, and inflammation.  
X Disclosure; SEQ ID NO 21; 140pp; English.  
CC The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.



XX	SQ	Sequence 184 AA;	RESULT 5
		Query Match 100.0%; Score 51; DB 3; Length 184;	AY71979 ID AAY71979 Standard; protein; 184 AA.
		Best Local Similarity 100.0%; Pred. No. 4.1e-47;	XX
		Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC
			XX
OY	1	MLQMAGCQCSQEYFDSSLHACTPCQLRCSNTPPTCQRCNASVTSVKG 51	DT 28-MAR-2001 (first entry)
Db	1	MLQMAGCQCSQEYFDSSLHACTPCQLRCSNTPPTCQRCNASVTSVKG 51	DE Human B cell maturation factor (BCMA) protein.
			XX
		Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;	XX
		KW Tumour necrosis factor and Apol- related leucocyte expressed Ligand 1;	KW
		ID AAE09241 standard; protein; 184 AA.	KW
		KW Tumour necrosis factor and Apol- related leucocyte expressed Ligand 1;	KW
		XX	therapay; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
		AAB09241;	KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
		XX	KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
		DT 19-NOV-2001 (first entry)	KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
		DE Human BCMA protein.	KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
		XX	KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
		OS Homo sapiens.	XX
		KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;	OS Homo sapiens.
		KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;	XX
		KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.	XX
		XX	Location/Qualifiers
		OS Homo sapiens.	PH 1 .62
		XX	/label= Extracellular_domain
		XX	PN WO200063378-A1.
		PN WO200160397-A1.	XX
		XX	PD 16-NOV-2000.
		PD 23-AUG-2001.	XX
		XX	PF 05-MAY-2000; 2000WO-US012266.
		PF 28-NOV-2000; 2000WO-US012378.	XX
		XX	PR 06-MAY-1999; 99US-0132892P.
		PR 16-FEB-2000; 2000US-0182938P.	XX
		PR 22-AUG-2000; 2000US-0226986P.	PR 01-MAY-2000; 2000US-0201012P.
		XX	PA (NBJE-) NAT JEWISH MEDICAL & RES CENT.
		XX	Shu HS;
		PI PI; 2001-016094/02.	XX
		PI PI; 2001-016094/02.	DR N-PSDB; AAD0125.
		XX	PT Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
		XX	PS Claim 37; Page 104-105; 112pp; English.
		XX	CC The present invention relates to Tumour necrosis factor (TNF) and Apol- related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.
		CC	CC The present sequence is a human B cell maturation factor (BCMA) protein.
		CC	CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
		CC	CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte maturation
		XX	Sequence 184 AA;
		SQ	Query Match 100.0%; Score 51; DB 4; Length 184;
			Best Local Similarity 100.0%; Pred. No. 4.1e-47;
			Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1	MLQMAGCQCSQEYFDSSLHACTPCQLRCSNTPPTCQRCNASVTSVKG 51	CC Sequence 184 AA;
Db	1	MLQMAGCQCSQEYFDSSLHACTPCQLRCSNTPPTCQRCNASVTSVKG 51	Query Match 100.0%; Score 51; DB 4; Length 184;
			Best Local Similarity 100.0%; Pred. No. 4.1e-47;
			Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
 CC immunosuppressive diseases, organ transplantation, inflammation and human  
 CC immunodeficiency virus (HTV), and for treating, suppressing or altering  
 CC an immune response involving a signalling pathway between APRIL-R and its  
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
 CC is human APRIL-R also referred as BCM or BCM protein.  
 XX Sequence 184 AA;  
 SQ

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51  
 Db 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51

RESULT 8  
 ID ABB81487  
 XX  
 AC ABB81487;  
 DT 02-SEP-2002 (first entry)  
 XX

DE Human BCM receptor related protein SEQ ID NO:7.  
 XX  
 KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;  
 KW immuno suppressive; dermatological; antiinflammatory; antidiabetic;  
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotopic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; graft rejection; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 PN WO200238766-A2.  
 PD 16-MAY-2002.  
 XX  
 PF 05-NOV-2001; 2001WO-US047018.  
 PR 07-NOV-2000; 2000US-0246449P.  
 PR 20-DEC-2000; 2000US-0257131P.  
 PR 28-JUN-2001; 2001US-0301715P.  
 PR 29-AUG-2001; 2001US-0315565P.  
 PA (ZYMO ) ZYMOGENETICS INC.

XX Gross JA, Xu W, Henne RM, Grant FJ;  
 XX DR WPI; 2002-508212/54.  
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed  
 PT ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
 PT renal failure or renal disease and lymphoma.  
 XX Disclosure; Page 135-136; 154pp; English.  
 XX The present invention describes a human tumour necrosis factor receptor  
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
 CC dermato logical, antiinflammatory, neuroprotective, antidiabetic,  
 CC antineuritic, antiarthritic, antiasthmatic, nephrotrophic, and hypotensive  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12  
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for

CC inhibiting the proliferation of tumour cells. (I) is useful for treating  
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia  
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal  
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host  
 CC disease, graft rejection and Crohn's disease. (I) is useful for  
 CC modulating the immune system, for regulating B cell responses and  
 CC development, for modulating development of other cells, antibody  
 CC production and cytokine production, and for modulating T and B cell  
 CC communication. The present sequence represents a protein which is given  
 XX in the exemplification of the present invention  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 51; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ID ABB54694;  
 XX  
 AC ABB54694;  
 DT 30-DEC-2002 (first entry)  
 XX Metastatic colorectal cancer-associated polypeptide.  
 DB 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.  
 Db 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.

RESULT 9

ABBP54694  
 ID. ABB54694 standard; protein; 184 AA.  
 XX  
 AC ABB54694;  
 DT 30-DEC-2002 (first entry)  
 XX Metastatic colorectal cancer-associated polypeptide.  
 DB 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.  
 Db 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.

Sequence 184 AA;

Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ID ABB54694;  
 XX  
 AC ABB54694;  
 DT 30-DEC-2002 (first entry)  
 XX Metastatic colorectal cancer-associated polypeptide.  
 DB 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.  
 Db 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.

XX  
 Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ID ABB54694;  
 XX  
 AC ABB54694;  
 DT 30-DEC-2002 (first entry)  
 XX Metastatic colorectal cancer-associated polypeptide.  
 DB 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.  
 Db 1 MLQWAGQCSQNEYFDLILHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51.

RESULT 9  
 ABP00268677-A2.  
 XX  
 PN WO200268677-A2.  
 XX  
 PD 06-SBP-2002.  
 XX  
 PP 27-FEB-2002; 2002WO-US006001.  
 XX  
 PR 27-FEB-2001; 2001US-0272206P.  
 PR 02-APR-2001; 2001US-0281149P.  
 PR 17-APR-2001; 2001US-0284555P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA (UICRA-) UNIV CASE WESTERN RESERVE.  
 XX  
 PI Mack DH, Markowitz SD;  
 XX  
 DR WPI; 2002-698677/75.  
 DR N-PSDB; ABQ81560.

XX  
 PS Claim 8; Page 255; 260pp; English.  
 XX  
 CC The present sequence is the protein sequence of a human polypeptide  
 CC encoded by a gene that exhibits decreased expression in colon cancer  
 CC derived metastases compared to normal colon tissue. It is an example of  
 CC claimed polypeptides that are encoded by genes which are differentially  
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are  
 CC useful in diagnostic and prognostic assays, for raising antibodies useful  
 e.g. in immunotherapy, and in screening for modulator compounds of  
 CC



Qy 1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51  
 ID ADA49361  
 AC ADA49361; 1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51  
 DB ADA49361 standard; protein; 184 AA.

## RESULT 12

ADA49361  
 ID ADA49361 standard; protein; 184 AA.  
 AC ADA49361;  
 XX 20-NOV-2003 (first entry)  
 DE Human BCMA protein.  
 XX human; TALL-1; antagonist; irrititic; antirheumatic;  
 XX antiinflammatory; antiarthritic; dermatological; antidiabetic;  
 XX neuroprotective; antithyroid; antipyretic; nephrotropic; vasotrophic;  
 XX autoimmune disease; nephrotic; arthritic;  
 XX systemic lupus erythematosus; insulin dependent diabetes mellitus;  
 XX multiple sclerosis; myasthenia gravis; Grave's disease;  
 XX autoimmune hemolytic anaemia; thrombocytopenic purpura;  
 XX Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;  
 XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.  
 OS Homo sapiens.  
 XX WO2003035846-A2.  
 XX PD 01-MAY-2003.  
 XX PP 24-OCT-2002; 2002WO-US034376.  
 XX PR 24-OCT-2001; 2001US-034516P.  
 PR 14-JAN-2002; 2002US-0348962P.  
 PR 07-FEB-2002; 2002US-0354965P.  
 PR 13-AUG-2002; 2002US-0403364P.  
 XX PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
 XX PI Zhang G, Shu H, Liu Y, Xu L;  
 XX DR WPI; 2003-403345/38.  
 DR N-PDB; ADA49360.  
 XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1 antagonist.  
 XX PS Claim 62; Page 613; 618pp; English.  
 XX The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:1, by at least one modification in the region connecting *&*; strands D and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, antiinflammatory, antiarthritic, dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents human BCMA.  
 XX SQ Sequence 184 AA;

Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51	1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51
Db	1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51	1 MLOMAGQCSQNEYFDSSLHACIPCQLRSSNTPLTCORYCNASVTVNSVKG 51

RESULT 13

ID	ABP60552	standard; protein; 184 AA.
XX	ABP60552;	
AC	ABP60552;	
XX	DT 28-MAR-2003	(first entry)
XX	XX	Human tumour necrosis factor BCMA.
XX	XX	APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
XX	XX	KW dermato logical; immunosuppressive; antiinflammatory; anti rheumatic; KW antiarthritis; cytotoxic; anti anaemic; antiallergic; anti asthmatic; KW neuroprotective; ophthalmological; tuberculous; anticabetic; KW antipsoriatic; anti HIV; anti arteriosclerotic; vaso tropic; thyromimetic; KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD; KW inflammatory disorder; proliferative disorder; single chain antibody; KW antibody; human; BCMA; tumour necrosis factor.
XX	XX	DE Homo sapiens.
XX	XX	WO20029192-A2.
PN	PN WO20029192-A2.	
XX	XX	PD 28-NOV-2002.
XX	XX	PP 22-MAY-2002; 2002WO-US016106.
XX	XX	PR 24-MAY-2001; 2001US-0293100P.
XX	XX	PA (HUMA-) HUMAN GENOME SCI INC.
XX	XX	PI Ruben SM;
XX	XX	DR WO2003-156740/15.
XX	XX	PT Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's syndrome.
XX	XX	PS Disclosure; Page 222; 225pp; English.
CC	CC	The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermatological, immunosuppressive, antiinflammatory, antirheumatic, antiarthritic, cytotoxic, anti anaemic, anti allergic, anti asthmatic, neuroprotective, ophthalmological, tuberculous, antidiabetic, antiparasitic, anti arteriosclerotic, vaso tropic, thyromimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in human, disease or disorder such as autoimmune disease, and graft versus host disease (GVHD). The autoimmune disease is systemic lupus erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody is useful for detecting, diagnosing, prognosis, treating, preventing or ameliorating a disease or disorder associated with aberrant APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL receptor. The disease or disorders includes autoimmune and inflammatory disorders such as autoimmune neuropropena, haemolytic anaemia, dermatitis, asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis, uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as myasthenia gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease, infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and proliferative disorders (e.g. leukemia). The present sequence represents

CC the tumour necrosis factor BCMA  
 XX Sequence 184 AA;

Query Match 100.0% ; Score 51; DB 6; Length 184; Best Local Similarity 100.0%; Pred. No. 4.1e-47; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DT 15-JAN-2004 (first entry) XX Human Ly1/32P protein SEQ ID NO:4.
---------------------------------------------------------------------------------------------------------------------------------------------------------------------	-----------------------------------------------------------------------

Qy 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51  
 Db 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51

RESULT 14

ABP97717 ID ABP97717 standard; protein; 184 AA. XX AC ABP97717; XX DT 28-MAY-2003 (first entry)	XX ABP97717 standard; protein; 184 AA. XX AC ABP97717; XX DT 28-MAY-2003 (first entry)
----------------------------------------------------------------------------------------------------------------	----------------------------------------------------------------------------------------------------

XX Amino acid sequence of human BCMA receptor.  
 XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus; BCMA.  
 XX OS Homo sapiens.  
 XX PN WO2003014294-A2.  
 XX PD 20-FEB-2003.  
 XX PF 24-JUL-2002; 2003WO-US023447.  
 XX PR 03-AUG-2001; 2001US-0310114P.  
 XX PR 30-APR-2002; 2002US-0377171P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PT Dixit V, Grewal I, Ridgway J, Yan M;  
 XX DR WPI; 2003-256560/25.  
 XX DR N-PSDB; ABZ68871.

New nucleic acid encoding a TAC1 or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus. Disclosure; Fig 2; 153pp; English.

The present sequence represents a human BCMA polypeptide. The specific sequence also describes TAC1 and BR3 polypeptides. TAC1 and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and APRIL bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to the BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus

Sequence 184 AA;

Query Match 100.0% ; Score 51; DB 6; Length 184; Best Local Similarity 100.0%; Pred. No. 4.1e-47; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DT 15-JAN-2004 (first entry) XX Human Ly1/32P protein SEQ ID NO:4.
---------------------------------------------------------------------------------------------------------------------------------------------------------------------	-----------------------------------------------------------------------

Qy 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51  
 Db 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51

RESULT 15

ADD67527 ID ADD67527 standard; protein; 184 AA. XX AC ADD67527; XX	Query Match 100.0% ; Score 51; DB 7; Length 184; Best Local Similarity 100.0%; Pred. No. 4.1e-47; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
--------------------------------------------------------------------------------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------

Qy 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51  
 Db 1 MLQAGGCSQNEYFDLILHACIPCQLRSSNTPPLTCRYCNASVTNSVKG 51

Search completed: March 2, 2006, 04:23:29  
 Job time : 187 secs

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Gencore version 5.1.7

OM protein - protein search, using SW model

Run on: March 2, 2006, 04:23:47 ; Search time 38 Seconds  
 (without alignments)  
 129.133 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51

Perfect score: 51

Sequence: 1 MLQAGQCSQNYYFDSSLHA.....TPPLTCQRYCNASTVNSVKG 51

Scoring-table: Oligo Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

## Post-processing: Listing first 45 summaries

Database : PIR 80.0  
 1: PIR;\*  
 2: PIR;\*  
 3: PIR;\*  
 4: PIR;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	51	100.0	184	2	S43496	B-cell maturation factor - human
2	7	13.7	309	2	E72365	conserved hypothetical protein
3	7	13.7	5188	2	B85547	probable RTX family
4	7	13.7	5291	2	F90695	hypothetical protein
5	6	11.8	113	2	B72242	hypothetical protein
6	6	11.8	129	2	A81187	type IV pilin protein
7	6	11.8	148	2	B58345	megakaryocyte - tremet
8	6	11.8	223	2	S16652	hypothetical protein
'9	6	11.8	237	2	T24407	hypothetical protein
10	6	11.8	240	2	A96697	protein F1N21.18
11	6	11.8	245	2	T36127	probable ribonuclease
12	6	11.8	249	2	T452217	rec7 protein - fibroblast
13	6	11.8	257	2	E89124	protein K07C11.1
14	6	11.8	269	2	AC0404	[probable deoR-family]
15	6	11.8	283	2	C86535	hypothetical protein
16	6	11.8	283	2	H72087	hypothetical protein
17	6	11.8	303	2	T17774	hypothetical protein
18	6	11.8	311	2	C69464	carboxylesterase
19	6	11.8	321	2	Q0BC15	[hypothetical protein]
20	6	11.8	321	2	F91104	hypothetical protein
21	6	11.8	321	2	A85950	probable membrane
22	6	11.8	327	2	S61660	conserved hypothetical protein
23	6	11.8	338	2	A82209	meiotic recombinant
24	6	11.8	339	2	T41126	hypothetical protein
25	6	11.8	340	2	B96632	(S)-2-hydroxy-acid
26	6	11.8	353	2	H75446	protein kinase (EC
27	6	11.8	398	1	OKBYC3	hypothetical protein
28	6	11.8	404	2	S64944	carbon monoxide de
29	6	11.8	406	2	H69095	conferred hypothetical protein - Thermotoga maritima (strain MSB8)

## ALIGNMENTS

## RESULT 1

S43496 - B-cell maturation factor - human  
 N;Alternate names: BCM protein; BCMA protein; BBL protein  
 C;Species: Homo sapiens (man)  
 C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S43486; S31208; E36661  
 R;Iaabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
 Nucleic Acids Res 22, 1147-1154, 1994  
 A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectional  
 A;Reference number: S43486; PMID:816126  
 A;Accession: S43486  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross references: UNIPARC:UPI0000034D1B; EMBL:Z14954; PIDN:CAA78679.1; PI  
 A;Residues: 1-184 <LA2>  
 A;Cross references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z229574; NID:9471244; PI  
 R;Iaabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
 EMBO J. 11, 3897-3904, 1992  
 A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;11)  
 A;Accession number: S31208; PMID:93010984  
 A;Accession: S31208  
 A;Molecule type: mRNA  
 A;Cross references: UNIPARC:UPI0000046868; EMBL:Z14955  
 A;Residues: 1-184 <LA2>  
 A;Accession: S36661  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Cross references: UNIPARC:UPI0000034D1B; EMBL:Z14955  
 A;Residues: 4-184 <LA3>  
 A;Cross references: UNIPARC:UPI0000046868; EMBL:Z14955  
 C;Genetics:  
 A;Gene: GDB:BCMA  
 A;Cross references: GDB:135577; OMIM:109545  
 A;Accession number: 1ep13.1-16p13.1  
 A;Introns: 44/1; 53/1  
 C;Superfamily: human B-cell maturation factor

Query Match Score 100.0%; Score 51; DB 2; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.e-47;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLQAGQCSQNYYFDSSLHACIPQLRCSSNTPLTCQRYCNAAVTNSVKG 51  
 Db 1 MLQAGQCSQNYYFDSSLHACIPQLRCSSNTPLTCQRYCNAAVTNSVKG 51.

RESULT 2

E72365 - conserved hypothetical protein - Thermotoga maritima  
 C;Species: Thermotoga maritima  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: E72355  
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.C.	
Nature 399, 323-329, 1999	
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence	
A;Reference number: A72200; MUID:99287116; PMID:10360571	
A;Accession: E72365	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-309 <ARN>	
A;Cross-references: UNIPROT:Q9WYX9; UNIPARC:UPI00000C13FC; GB:AE001728; GB:AE000512; NID:050952	
A;Experimental source: strain MSB8	
C;Genetics:	
A;Gene: TM0519	
Query Match Score 7; DB 2; Length 309; Best Local Similarity 100.0%; Pred. No. 6.2; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 12 EYFDSSL 18 Db 165 EYFDSSL 171	
RESULT 3	
B85547 probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #text_change 09-Jul-2004	
C;Accession: B85547 R;Parra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glazner, J.D.; Rose, D.J.; Mayhew, L.; Grotnes, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001	
A;Title: Genomic sequence of enterohemorrhagic Escherichia coli O157:H7.	
A;Reference number: A85480; MUID:21074935; PMID:11206551	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-5188 <STO>	
A;Cross-references: UNIPROT:Q8X4H5; UNIPARC:UPI000011021E; GB:AE005174; NID:912513368; F	
A;Experimental source: strain O157:H7, substrain EDL933	
C;Genetics:	
A;Gene: 20615	
Query Match Score 7; DB 2; Length 5188; Best Local Similarity 100.0%; Pred. No. 72; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 43 ASVTSV 49 Db 1814 ASVTSV 1820	
RESULT 4	
F90696 hypothetical protein EC80542 [imported] - Escherichia coli (strain O157:H7, substrain RI;Species: Escherichia coli C;Date: 18-Jul-2001 #text_change 09-Jul-2004	
C;Accession: F90696 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;Gotoh, N.; Yasunaga, T.; Khara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
DNA Res. 8, 11-22, 2001	
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796	
A;Accession: F90696	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-5291 <HAY>	
A;Cross-references: UNIPROT:Q8X2T1; UNIPARC:UPI000011021F; GB:BA000007; FIDN:BAB33965-1; NID:050952	
A;Experimental source: strain O157:H7, substrain RIMD 050952	
C;Genetics:	
A;Gene: EC80542	
Query Match Score 7; DB 2; Length 5291;	

C;Species: Isoparorchis hypselobagri  
 C;Date: 23-May-1997 #sequence\_revision 23-May-1997 #text\_change 12-Jul-2004  
 C;Accession: B58345  
 R;Rashid, A.R.; Van Hauwaert, M.; Hague, M.; Siddiqi, A.H.; Lasters, I.; De Mayer, M.; C  
 Submitted to the Protein Sequence Database, October 1996  
 A;Description: Trematode myoglobins: functional molecules with a distal tyrosine.  
 A;Reference number: A58345  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-148 <RAS>  
 A;Cross-references: UNIPROT:P80722; UNIPARC:UPI000012B54D  
 A;Note: monomeric myoglobin with tyrosine at position B10 and E7 (distal position) res  
 C;Superfamily: trematode myoglobin; globin homology

Query Match 11.8%; Score 6; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FDSLH 19  
 Db 7 FDSLH 12

RESULT 8  
 S16652 hypothetical protein\_223 - Escherichia coli retron Bc86  
 C;Species: Escherichia coli retron Bc86  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 17-Jul-1998  
 C;Accession: S16652  
 R;Lim, D.  
 Mol. Microbiol. 5, 1863-1872, 1991  
 A;Title: Structure of two retrons of *Escherichia coli* and their common chromosomal inser  
 A;Reference number: S16652; MUID:92114764; PMID:1722556  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-223 <LIM>  
 A;Cross-references: UNIPARC:UPI000017CAC0; EMBL:X60206  
 A;Experimental source: strain B

Query Match 11.8%; Score 6; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 LRCSSN 31  
 Db 152 LRCSSN 157

RESULT 9  
 T24407 hypothetical protein T01F7.6 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T24407  
 R;Morlmore, B.  
 Submitted to the EMBL Data Library, June 1996  
 A;Reference number: Z19887  
 A;Accession: T24407  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-237 <WIL>  
 A;Cross-references: UNIPROT:Q22118; UNIPARC:UPI00000827F9; EMBL:Z74041; PIDN:CAA98521.1;  
 A;Experimental source: clone T03F7  
 A;Gene: CESP:T03F7.6  
 A;Map position: 5  
 A;Introns: 12/1; S3/1; 117/3; 168/3; 191/3

Query Match 11.8%; Score 6; DB 2; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CNASVT 46  
 Db 40 CNASVT 45

RESULT 12  
 T45217 rec7 protein - fission yeast (*Schizosaccharomyces pombe*)  
 C;Species: *Schizosaccharomyces pombe*

C; Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C; Accession: T42217  
 R; Lin, Y.  
 Genetics 132, 75-85, 1992  
 A; Title: Meiotically induced rec7 and rec8 Schizosaccharomyces pombe genes.  
 A; Reference number: Z22941; MUID:1339382  
 A; Accession: T45217  
 A; Status: preliminary; translated from GB/EMBL/DDDBJ  
 A; Molecule type: DNA  
 A; Residues: 1-249 <LIN>  
 A; Cross-references: UNIPARC:UPI000017B220; EMBL:M85297; NID:9173451; PIDN:AAA35333.1; PI  
 C; Genetics:  
 A; Gene: rec7  
 C; Function:  
 A; Description: required for meiotic intragenic recombination but not for mitotic recombination  
 Query Match 11.8%; Score 6; DB 2; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 30 SNTPP 35  
 Db 110 SNTPP 115

RESULT 13  
 B89124 protein K07C11.1 [imported] - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C; Accession: E89124  
 R; anonymous, The C. elegans Sequencing Consortium.  
 Science 2012-2018, 1998  
 A; Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
 A; Reference number: A75000; MUID:99069613; PMID:9851916  
 A; Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
 A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A; Accession: E89124  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-257 <STO>  
 A; Cross-references: UNIPROT:Q21272; UNIPARC:UPI0000077A84; GB:chr\_V; PIDN:AAA96181.1; PI  
 C; Genetics:  
 A; Gene: K07C11.1  
 A; Map Position: 5  
 C; Superfamily: paired box transcription factor Pax-8; paired box homology

Query Match 11.8%; Score 6; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 SSNTPP 34  
 Db 242 SSNTPP 247

RESULT 14  
 AC0404 probable deer-f family regulatory protein YPO3327 [imported] - *Yersinia pestis* (strain CO9  
 C; Species: *Yersinia pestis*  
 C; Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C; Accession: AC0404  
 R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
 deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A; Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A; Reference number: AB0001; MUID:21470413; PMID:11586360  
 A; Accession: AC0404  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-269 <KOB>  
 A; Cross-references: UNIPROT:Q8ZBS6; UNIPARC:UPI00000DC895; GB:AL590842; PIDN:CAC92559.1;

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GenCore version 5.1.7

## OM protein - protein search, using SW model

Run on: March 2, 2006, 04:38:58 ; Search time 164 Seconds

(without alignments)

129.935 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51

Perfect score: 51

Sequence: 1 MLQAGQCSENEYFDSSLHAA.....TPPLTCQRVCNASTVNSVKG 51

Scoring-table: OTIGO

Gapext: 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 8, Max size: 0  
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:  
 1: /cn2\_6\_ptodata/1/pubpa/us07\_pubcomb.pep\*  
 2: /cn2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep\*  
 3: /cn2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep\*  
 4: /cn2\_6\_ptodata/1/pubpa/us10\_pubcomb.pep\*  
 5: /cn2\_6\_ptodata/1/pubpa/us11\_pubcomb.pep\*  
 6: /cn2\_6\_ptodata/1/pubpa/us11\_pubcomb.pep\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	4	US-10-077-438-1
2	51	100.0	184	4	US-10-077-438-7
3	51	100.0	184	4	US-10-077-137-1
4	51	100.0	184	4	US-10-077-137-7
5	51	100.0	184	4	US-10-068-725-2
6	51	100.0	184	4	US-10-151-882-47
7	51	100.0	184	4	US-10-115-192-8
8	51	100.0	184	4	US-10-008-063-7
9	51	100.0	184	4	US-10-152-363A-27
10	51	100.0	184	4	US-10-216-074-11
11	51	100.0	184	4	US-10-087-080-39
12	51	100.0	184	4	US-10-742-034-9
13	51	100.0	184	5	US-10-626-014-6
14	51	100.0	184	5	US-10-485-489-6
15	51	100.0	184	5	US-10-861-049-27
16	51	100.0	184	5	US-10-989-826-46
17	51	100.0	184	6	US-11-021-874-27
18	51	100.0	302	4	US-10-115-192-12
19	48	94.1	51	3	US-09-854-864-6
20	48	94.1	51	3	US-09-855-158-6
21	48	94.1	181	3	US-09-854-064-5
22	48	94.1	181	3	US-09-855-158-5
23	48	94.1	283	3	US-09-854-064-9
24	48	94.1	283	3	US-09-855-158-9
25	44	86.3	58	3	US-09-855-158-21
26	44	86.3	58	3	US-09-855-158-21
27.	37	72.5	207	4	US-10-077-438-3

## ALIGNMENTS

RESULT 1  
US-10-077-438-1  
; Sequence 1, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Thompson, Jeffrey  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Apotech R&D S.A.  
; TITLE OF INVENTION: Baff Receptor (BCMA), An Immunoregulatory Agent  
; FILE REFERENCE: A080PCT  
; CURRENT APPLICATION NUMBER: US/10/077-438  
; CURRENT FILING DATE: 2002-02-18  
; PRIORITY APPLICATION NUMBER: 60/149,378  
; PRIORITY FILING DATE: 1999-08-17  
; PRIORITY APPLICATION NUMBER: 60/181,684  
; PRIORITY FILING DATE: 2000-02-11  
; PRIORITY APPLICATION NUMBER: 60/183,536  
; PRIORITY FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: homo sapien  
; PRIOR FILING DATE: 2000-02-11  
; US-10-077-438-1

Query Match Similarity Best Local Similarity Score 51; DB 4; Length 184;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 2  
US-10-077-438-7  
; Sequence 7, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Tschopp, Jurg

APPLICANT: Schneider, Pascal  
 APPLICANT: Thompson, Jeffrey  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Apotech R&D S.A.  
 TITLE OF INVENTION: Baff Receptor (BCMA), An Immunoregulatory Agent  
 FILE REFERENCE: A080PCT  
 CURRENT APPLICATION NUMBER: US/10/077,438  
 CURRENT FILING DATE: 2002-02-18  
 PRIOR APPLICATION NUMBER: 60/149,378  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/181,684  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: 60/183,536  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: homo sapien  
 US-10-077-138-7

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Software: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 184  
 ORGANISM: homo sapien  
 US-10-077-138-7

RESULT 3  
 US-10-077-137-1  
 Sequence 1, Application US/10077137  
 Publication No. US20020172674A1  
 GENERAL INFORMATION:  
 APPLICANT: Mackay, Fabienne  
 APPLICANT: Browning, Jeffrey  
 APPLICANT: Ambrose, Christine  
 APPLICANT: Techopp, Jurg  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Thompson, Jeffrey  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Apotech R&D S.A.

TITLE OF INVENTION: Baff Receptor (BCMA), An Immunoregulatory Agent  
 FILE REFERENCE: A080PCT  
 CURRENT APPLICATION NUMBER: US/10/077,137  
 CURRENT FILING DATE: 2002-02-15  
 PRIOR APPLICATION NUMBER: 60/149,378  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/181,684  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: 60/183,536  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: homo sapien  
 US-10-077-137-1

RESULT 4  
 US-10-077-137-7  
 Sequence 7, Application US/10077137  
 Publication No. US20020172674A1  
 GENERAL INFORMATION:  
 APPLICANT: Mackay, Fabienne  
 APPLICANT: Browning, Jeffrey  
 APPLICANT: Ambrose, Christine  
 APPLICANT: Techopp, Jurg  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Thompson, Jeffrey  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Apotech R&D S.A.  
 TITLE OF INVENTION: Baff Receptor (BCMA), An Immunoregulatory Agent  
 FILE REFERENCE: A080PCT  
 CURRENT APPLICATION NUMBER: US/10/077,137  
 CURRENT FILING DATE: 2002-02-15  
 PRIOR APPLICATION NUMBER: 60/149,378  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/181,684  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: 60/183,536  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: homo sapien  
 US-10-077-138-7

RESULT 5  
 US-10-068-725-2  
 Sequence 2, Application US/10068725  
 Publication No. US2003012733A1  
 GENERAL INFORMATION:  
 APPLICANT: Kindtbrogel, Wayne  
 TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI  
 FILE REFERENCE: 01-04  
 CURRENT APPLICATION NUMBER: US/10/068,725  
 CURRENT FILING DATE: 2002-02-06  
 PRIOR APPLICATION NUMBER: 60/270,274  
 PRIOR FILING DATE: 2001-02-20  
 PRIOR APPLICATION NUMBER: 60/283,447  
 PRIOR FILING DATE: 2001-04-12  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-068-725-2

RESULT 6  
 Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Software: FastSEQ for Windows Version 3.0  
 SEQ ID NO 1  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-068-725-1

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Software: FastSEQ for Windows Version 3.0  
 SEQ ID NO 1  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-068-725-2

US-10-151-882-47  
*; Sequence 47, Application US/10151882*  
*; GENERAL INFORMATION*  
*; APPLICANT: Ruben, Steven M.*  
*; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRII)*  
*; FILE REFERENCE: PF54*  
*; CURRENT APPLICATION NUMBER: US/10/151, 882*  
*; CURRENT FILING DATE: 2002-05-22*  
*; PRIOR APPLICATION NUMBER: 60/293, 100*  
*; PRIORITY FILING DATE: 2001-05-24*  
*; NUMBER OF SEQ ID NOS: 48*  
*; SOFTWARE: Patentin version 3.0*  
*; SEQ ID NO: 47*  
*; LENGTH: 184*  
*; TYPE: PRT*  
*; ORGANISM: Homo sapiens*  
*US-10-151-882-47*

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 US-10-115-1192-8  
*; Sequence 8, Application US/10115192*  
*; Publication No. US20030082175A1*  
*; GENERAL INFORMATION*  
*; APPLICANT: Apotech R & D S.A.*  
*; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof*  
*; FILE REFERENCE: A033CT*  
*; CURRENT APPLICATION NUMBER: US/10/115, 192*  
*; CURRENT FILING DATE: 2002-04-02*  
*; PRIOR APPLICATION NUMBER: 60/215688*  
*; PRIOR FILING DATE: 2000-06-30*  
*; PRIOR APPLICATION NUMBER: 60/181807*  
*; PRIOR FILING DATE: 2000-02-11*  
*; PRIOR APPLICATION NUMBER: 60/157933*  
*; PRIOR FILING DATE: 1999-10-06*  
*; NUMBER OF SEQ ID NOS: 12*  
*; SOFTWARE: FastSEQ for Windows Version 4.0*  
*; SEQ ID NO: 8*  
*; LENGTH: 184*  
*; TYPE: PRT*  
*; ORGANISM: homo sapiens*  
*US-10-115-1192-8*

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 US-10-008-063-7  
*; Sequence 7, Application US/10008063*  
*; Publication No. US20030092164A1*  
*; GENERAL INFORMATION*  
*; APPLICANT: Gross, Jane A.*  
*; APPLICANT: Henne, Randal M.*  
*; APPLICANT: Grant, Francis, J.*  
*; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor*  
*; FILE REFERENCE: 00-103*

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 US-10-152-363A-27  
*; Sequence 27, Application US/10152363A*  
*; Publication No. US20030103986A1*  
*; GENERAL INFORMATION*  
*; APPLICANT: Rixon, Mark W.*  
*; APPLICANT: Gross, Jane A.*  
*; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins*  
*; FILE REFERENCE: 01-20*  
*; CURRENT APPLICATION NUMBER: US/10/152, 363A*  
*; CURRENT FILING DATE: 2002-05-20*  
*; PRIOR APPLICATION NUMBER: 60/293, 343*  
*; PRIOR FILING DATE: 2001-05-24*  
*; NUMBER OF SEQ ID NOS: 70*  
*; SEQ ID NO: 27*  
*; SOFTWARE: FastSEQ for Windows Version 3.0*  
*; LENGTH: 184*  
*; TYPE: PRT*  
*; ORGANISM: Homo sapiens*  
*US-10-152-363A-27*

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 US-10-216-074-11  
*; Sequence 11, Application US/10216074*  
*; Publication No. US20030148445A1*  
*; GENERAL INFORMATION*  
*; APPLICANT: Shu, Hong-Bing*  
*; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF*  
*; FILE REFERENCE: 2879-72*  
*; CURRENT APPLICATION NUMBER: US/10/216, 074*  
*; CURRENT FILING DATE: 2003-03-12*  
*; PRIOR APPLICATION NUMBER: US/09/565, 423*  
*; PRIOR FILING DATE: 2000-05-05*  
*; PRIOR APPLICATION NUMBER: UNKNOWN*  
*; PRIOR FILING DATE: 2000-05-01*  
*; PRIOR APPLICATION NUMBER: 60/132, 892*  
*; NUMBER OF SEQ ID NOS: 17*  
*; SOFTWARE: PatentIn Ver. 2.1*  
*; SEQ ID NO: 11*  
*; LENGTH: 184*  
*; TYPE: PRT*  
*; ORGANISM: Homo sapiens*  
*US-10-216-074-11*

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ORGANISM: Homo sapiens  
 US-10-742-634-9

Qy 1 MLQAGGQSNEYFDSLHACIPCQLRCSNTTPPLTCQRYCNASVTNSVKG 51  
 Db 1 MLQAGGQSNEYFDSLHACIPCQLRCSNTTPPLTCQRYCNASVTNSVKG 51

RESULT 11  
 Sequence 3.9, Application US/10087080  
 Publication No. US2003035820A1  
 GENERAL INFORMATION:  
 APPLICANT: Mack, David H.  
 APPLICANT: Markowitz, Sanford David  
 APPLICANT: Bos Biotechnology, Inc.  
 APPLICANT: Case Western Reserve University  
 TITLE OF INVENTION: No. US2003025820A1el Methods of Diagnosis of Metastatic Colorectal Cancer  
 TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for  
 Modulators of Metastatic Colorectal Cancer  
 FILE REFERENCE: 016501-00084US  
 CURRENT APPLICATION NUMBER: US/10/087.080  
 PRIOR APPLICATION NUMBER: US 60/272,206  
 PRIOR FILING DATE: 2002-10-25  
 PRIOR APPLICATION NUMBER: US 60/281,149  
 PRIOR FILING DATE: 2001-04-02  
 PRIOR APPLICATION NUMBER: US 60/284,555  
 PRIOR FILING DATE: 2001-04-17  
 NUMBER OF SEQ ID NOS: 41  
 SEQ ID NO 39  
 LENGTH: 184  
 FEATURE: tumor necrosis factor receptor superfamily, member  
 OTHER INFORMATION: 17 (TNFRSF17)  
 OTHER INFORMATION: tumor necrosis factor receptor superfamily, member  
 OTHER INFORMATION: 17 (TNFRSF17)

Query Match 100.0%; Score 51; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ORGANISM: Homo sapiens  
 US-10-087-080-39

Qy 1 MLQAGGQSNEYFDSLHACIPCQLRCSNTTPPLTCQRYCNASVTNSVKG 51  
 Db 1 MLQAGGQSNEYFDSLHACIPCQLRCSNTTPPLTCQRYCNASVTNSVKG 51

RESULT 12  
 US-10-742-634-9  
 Sequence 9, Application US/10742634  
 Publication No. US2004020882A1  
 GENERAL INFORMATION:  
 APPLICANT: Parmelee, David  
 APPLICANT: Yeh, Ben-Hwa  
 APPLICANT: Galperina, Olga  
 APPLICANT: Hilbert, David  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Thereof  
 CURRENT APPLICATION NUMBER: US/10/742,634  
 CURRENT FILING DATE: 2003-12-22  
 PRIOR APPLICATION NUMBER: US 60/435,262  
 PRIOR APPLICATION NUMBER: US 60/467,198  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 9  
 LENGTH: 184

Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 US-10-626-914-6  
 Sequence 6, Application US/10626914  
 Publication No. US20050043516A1  
 GENERAL INFORMATION:  
 Patin Docket Preview  
 APPLICANT: CHUNTHARAPAI, ANAN  
 APPLICANT: GREWAL, TOBAL  
 APPLICANT: KIM, KYUNG JIN  
 APPLICANT: YAN, MINHONG  
 TITLE OF INVENTION: TACI Antibodies and Uses Thereof  
 FILE REFERENCE: P1942A1  
 CURRENT APPLICATION NUMBER: US/10/626,914  
 CURRENT FILING DATE: 2003-07-25  
 PRIOR APPLICATION NUMBER: US 60/398,530  
 PRIOR FILING DATE: 2002-07-25  
 NUMBER OF SEQ ID NOS: 17  
 SEQ ID NO 6  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-626-914-6

Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 US-10-485-489-6  
 Sequence 6, Application US/10485489  
 Publication No. US20050070589A1  
 GENERAL INFORMATION:  
 APPLICANT: Dixit, Vibava  
 APPLICANT: Grewal, Tobal  
 APPLICANT: Ridgway, John  
 APPLICANT: Yan, Minhong  
 TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof  
 FILE REFERENCE: 11669\_175JSWO  
 CURRENT FILING DATE: 2004-01-30  
 PRIOR APPLICATION NUMBER: PCT/US02/23487  
 PRIOR FILING DATE: 2002-07-24  
 PRIOR APPLICATION NUMBER: US 60/310,114  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: US 60/377,171  
 SEQ ID NO 6  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-485-489-6

Query Match 100.0%; Score 51; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 MLQAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 51
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Db   1 MLQAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 51
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15

US-10-861-049-27

; Sequence 27, Application US/10861049

; PUBLICATION NO. US20050095243A1

; GENERAL INFORMATION:

; APPLICANT: Andrew Chan

; APPLICANT: Qian Gong

; APPLICANT: Flavious Martin

; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

; FILE REFERENCE: P2040RIUS

; CURRENT APPLICATION NUMBER: US/10/861,049

; CURRENT FILING DATE: 2004-06-04

; PRIOR APPLICATION NUMBER: US 60/476,531

; PRIOR FILING DATE: 2003-06-06

; PRIOR APPLICATION NUMBER: US 60/476,481

; PRIOR FILING DATE: 2003-06-05

; PRIOR APPLICATION NUMBER: US 60/476,414

; PRIOR FILING DATE: 2003-06-05

; NUMBER OF SEQ ID NOS: 145

; SEQ ID NO 27

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-861-049-27

Query Match 100.0%; Score 51; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 3.1e-45;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 MLQAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 51
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1 MLQAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 51
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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 Job time : 165 secs

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OM protein - protein search, using SW model

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(without alignments)

48.572 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51

Perfect score: 51

Sequences: 1 MLQAGQCSONEYFDSLHAA.....TPPJTQCRCNASTVNSVKG 51

Scoring Table: Oligo Gapex 60.0 , Gapext 60.0

Searched: 135339 seqs, 20000136 residues

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Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:  
 1: /cnr2\_6\_ptodata/2/pubpa/us08\_new\_pub.pep;  
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 3: /cnr2\_6\_ptodata/2/pubpa/us07\_new\_pub.pep;  
 4: /cnr2\_6\_ptodata/2/pubpa/pct\_new\_pub.pep;  
 5: /cnr2\_6\_ptodata/2/pubpa/us05\_new\_pub.pep;  
 6: /cnr2\_6\_ptodata/2/pubpa/us10\_new\_pub.pep;  
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 8: /cnr2\_6\_ptodata/2/pubpa/us01\_new\_pub.pep;

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	6 US-10-742-634-9	Sequence 9, App1
2	51	100.0	184	6 US-10-967-527A-8	Sequence 8, App1
3	51	100.0	184	7 US-11-0967-527A-7	Sequence 27, App1
4	40	78.4	40	6 US-10-967-527A-9	Sequence 9, App1
5	10	19.6	185	6 US-10-967-527A-10	Sequence 10, App1
6	7	13.7	5291	7 US-11-052-554A-281	Sequence 281, App1
7	6	11.8	231	7 US-11-10-183-37	Sequence 37, App1
8	6	11.8	313	7 US-11-098-686-10357	Sequence 1057, App1
9	6	11.8	379	7 US-11-072-512-3298	Sequence 328, App1
10	6	11.8	398	7 US-11-132-142-7	Sequence 7, App1
11	6	11.8	572	7 US-11-072-512-3907	Sequence 1407, App1
12	6	11.8	605	6 US-10-689-742-140	Sequence 5101, App1
13	6	11.8	668	7 US-11-087-099-5101	Sequence 5101, App1
14	6	11.8	766	6 US-10-821-234-1691	Sequence 1691, App1
15	6	11.8	800	7 US-11-072-512-2534	Sequence 3534, App1
16	6	11.8	1137	7 US-11-012-162-70	Sequence 70, App1
17	6	11.8	1461	7 US-11-052-554A-283	Sequence 283, App1
18	6	11.8	5405	7 US-11-10-172-1116	Sequence 1116, App1
19	5	9.8	8	7 US-11-045-024-196	Sequence 4967, App1
20	5	9.8	8	7 US-11-045-024-1697	Sequence 1697, App1
21	5	9.8	8	7 US-11-045-024-1698	Sequence 1698, App1
22	5	9.8	8	7 US-11-045-024-3636	Sequence 3636, App1
23	5	9.8	8	7 US-11-045-024-4379	Sequence 4379, App1
24	5	9.8	8	7 US-11-045-024-4380	Sequence 4380, App1
25	5	9.8	8	7 US-11-045-024-6787	Sequence 6787, App1

## ALIGNMENTS

RESULT 1  
US-10-742-634-9  
 Sequence 9, Application US/10742634  
 ; Publication No. US20050249671A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parmelee, David  
 ; Yeh, Ren-Hwa  
 ; APPLICANT: Galperina, Olga  
 ; APPLICANT: Hilbert, David  
 ; APPLICANT: Robien, Craig A.  
 ; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses T  
 ; FILE REFERENCE: 1488-1810002  
 ; CURRENT FILING DATE: 2003-12-22  
 ; PRIORITY APPLICATION NUMBER: US 10/742,634  
 ; PRIORITY FILING DATE: 2002-12-23  
 ; PRIORITY APPLICATION NUMBER: US 60/467,198  
 ; PRIORITY FILING DATE: 2003-05-02  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 184  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-742-634-9

Query Match 100.0%; Score 51; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 8.3-e-48;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSONEYFDSLHACIPOQLRSSNTPLTCORYCNASVTNSVKG 51  
 Db 1 MLQAGQCSONEYFDSLHACIPOQLRSSNTPLTCORYCNASVTNSVKG 51

RESULT 2  
US-10-967-527A-8  
 Sequence 8, Application US/10967527A  
 ; Publication No. US20050256041A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox, Brian A.  
 ; APPLICANT: Hollaway, James L.  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: Ztnf14, A Tumor Necrosis Factor  
 ; FILE REFERENCE: 03-17  
 ; CURRENT APPLICATION NUMBER: US/10/967,527A  
 ; CURRENT FILING DATE: 2004-10-18

PRIOR APPLICATION NUMBER: 60/511,698  
 PRIOR FILING DATE: 2003-10-16  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 8  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-967-527A-8

Qy \* 1 MLQAGGQCSQEYFDLILHACIPCQLRSNTTPLTCRYCNASVTNSVKG 51  
 Db \* 1 MLQAGGQCSQEYFDLILHACIPCQLRSNTTPLTCRYCNASVTNSVKG 40

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RESULT 3  
 US-11-242-294-27  
 Sequence 27, Application US/11242294  
 Publication No. US20060034852A1  
 GENERAL INFORMATION:  
 APPLICANT: Rixon, Mark W.  
 APPLICANT: Gross, Jane A.  
 TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
 FILE REFERENCE: 01-20  
 CURRENT APPLICATION NUMBER: US/11/242.294  
 CURRENT FILING DATE: 2005-10-03  
 PRIOR APPLICATION NUMBER: US/10/152,363  
 PRIOR FILING DATE: 2002-05-20  
 PRIOR APPLICATION NUMBER: 60/293,343  
 PRIOR FILING DATE: 2001-05-24  
 NUMBER OF SEQ ID NOS: 70  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 27  
 LENGTH: 184  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-242-294-27

Query Match 100.0%; Score 51; DB 7; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
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Qy \* 1 MLQAGGQCSQEYFDLILHACIPCQLRSNTTPLTCRYCNASVTNSVKG 51  
 Db \* 1 MLQAGGQCSQEYFDLILHACIPCQLRSNTTPLTCRYCNASVTNSVKG 51

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RESULT 4  
 US-10-967-527A-9  
 Sequence 9, Application US/10967527A  
 Publication No. US20050256041A1  
 GENERAL INFORMATION:  
 APPLICANT: Fox, Brian A.  
 APPLICANT: Holloway, James L.  
 APPLICANT: Sheppard, Paul O.  
 TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor  
 TITLE OF INVENTION: Receptor  
 FILE REFERENCE: 03-17  
 CURRENT APPLICATION NUMBER: US/10/967,527A  
 CURRENT FILING DATE: 2004-10-18  
 PRIOR APPLICATION NUMBER: 60/511,698  
 PRIOR FILING DATE: 2003-10-16  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 9  
 LENGTH: 40  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 FEATURE:

Query Match 100.0%; Score 7; DB 7; Length 5291;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ASVTNSV 49  
 Db 1814 ASVTNSV 1820

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**RESULT 7**  
 US-11-100-183-37  
 ; Sequence 37, Application US/1100183  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRATEGENE California  
 ; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription  
 ; FILE REFERENCE: 25436/2452 US/11/100,183  
 ; CURRENT APPLICATION NUMBER: US/11/100,183  
 ; CURRENT FILING DATE: 2005-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/559,810  
 ; PRIOR FILING DATE: 2004-04-06  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 37  
 ; LENGTH: 231  
 ; TYPE: PRT  
 ; ORGANISM: Bordetella pertussis  
 US-11-100-183-37

Query Match 11.8%; Score 6; DB 7; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 15 DSSLHA 20  
 Db 118 DSSLHA 123

**RESULT 8**  
 US-11-098-686-10357  
 ; Sequence 10357, Application US/11098686  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND POLYPEPTIDE SEQUENCES  
 ; FILE REFERENCE: 09531-128001  
 ; CURRENT APPLICATION NUMBER: US/11/098,686  
 ; CURRENT FILING DATE: 2005-04-04  
 ; PRIOR APPLICATION NUMBER: PCT/US03/31318  
 ; PRIOR FILING DATE: 2003-10-01  
 ; PRIOR APPLICATION NUMBER: US 60/416,395  
 ; PRIOR FILING DATE: 2002-10-04  
 ; NUMBER OF SEQ ID NOS: 11433  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO: 10357  
 ; LENGTH: 313  
 ; TYPE: PRT  
 ; ORGANISM: Lawsonia intracellularis  
 US-11-098-686-10357

Query Match 11.8%; Score 6; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 43 ASVTNS 48  
 Db 135 ASVTNS 140

---

; APPLICANT: OTSUKI, TETSUJI  
 ; APPLICANT: WAKAMATSU, AI  
 ; APPLICANT: SATO, HIROYUKI  
 ; APPLICANT: ISHII, SHIZUKO  
 ; APPLICANT: YAMAMOTO, JUN-ICHI  
 ; APPLICANT: ISONO, YUKO  
 ; APPLICANT: HIO, YURI  
 ; APPLICANT: OTSUKA, KAORU  
 ; APPLICANT: NAGAI, KEIICHI  
 ; APPLICANT: IRIE, RYOTARO  
 ; APPLICANT: TABUCHIKI, ICHIRO  
 ; APPLICANT: SAKI, NAOHTO  
 ; APPLICANT: YOSHIKAWA, TSUTOMU  
 ; APPLICANT: OTSUKA, MOTOKI  
 ; APPLICANT: NAGAHARI, KENJI  
 ; APPLICANT: MASUHO, YASUHIKO  
 ; TITLE OF INVENTION: Novel full length cDNA  
 ; FILE REFERENCE: 084335-0191  
 ; CURRENT APPLICATION NUMBER: US/11/072,512  
 ; CURRENT FILING DATE: 2005-03-07  
 ; PRIOR APPLICATION NUMBER: US 60/350,978  
 ; PRIOR FILING DATE: 2002-01-25  
 ; PRIOR APPLICATION NUMBER: JP 2001-379298  
 ; PRIOR FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 4096  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 3298

Query Match 11.8%; Score 6; DB 7; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 12 EYFSNL 17  
 Db 163 EYFSNL 168

---

**RESULT 10**  
 US-11-132-142-7  
 ; Sequence 7, Application US/11132142  
 ; Publication No. US2005026818A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Burnham Institute  
 ; APPLICANT: Silmora, Sergey  
 ; APPLICANT: Godzik, Adam  
 ; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A TARGET FOR SARS THERAPY  
 ; FILE REFERENCE: 8014-011-US  
 ; CURRENT APPLICATION NUMBER: US/11/132,142  
 ; CURRENT FILING DATE: 2005-05-17  
 ; PRIOR APPLICATION NUMBER: 60/571,698  
 ; PRIOR FILING DATE: 2004-05-17  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 7  
 ; LENGTH: 398  
 ; TYPE: PRT  
 ; ORGANISM: Saccharomyces sp.  
 ; SEQ ID NO: 11  
 ; LENGTH: 398

Query Match 11.8%; Score 6; DB 7; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 28 CSSNTP 33  
 Db 42 CSSNTP 47

---

**RESULT 9**  
 US-11-072-512-3298  
 ; Sequence 3298, Application US/11072512  
 ; Publication No. US20060229945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISOGAI, TAKAO  
 ; APPLICANT: SUGIYAMA, TOMOYASU

RESULT 11  
US-11-072-512-3-907  
Sequence 3907, Application US/11072512  
Publication No. US2006029945A1  
GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YURU  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KOROU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOKI  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASURO, YASUHIKO  
TITLE OF INVENTION: Novel, full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 3907  
LENGTH: 572  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-072-512-3-907  
Query Match 11.8%; Score 6; DB 7; Length 572;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 12 BYFDSL 17  
Db 163 BYFDSL 168

RESULT 12  
US-10-689-742-140  
Sequence 140, Application US/10689742  
Publication No. US20050250180A1  
GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: LaValle, Edward R  
; APPLICANT: Racine, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vicki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: 00766.000091.10  
CURRENT APPLICATION NUMBER: US/10/689,742  
CURRENT FILING DATE: 2003-10-22  
PRIOR APPLICATION NUMBER: 09/746,783  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 140  
LENGTH: 605  
TYPE: PRT  
ORGANISM: Homo sapiens

RESULT 13  
US-11-087-099-5101  
Sequence 5101, Application US/11087099  
Publication No. US200601961A1  
GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(5445) B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO: 5101  
LENGTH: 668  
TYPE: PRT  
ORGANISM: Petunia x hybrida  
US-11-087-099-5101  
Query Match 11.8%; Score 6; DB 7; Length 668;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 29 SSNTPP 34  
Db 216 SSNTPP 221

RESULT 14  
US-10-321-234-1691  
Sequence 1691, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/321,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIORITY NUMBER: US 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SEQ ID NO: 1691  
; LENGTH: 766  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1691  
Query Match 11.8%; Score 6; DB 6; Length 766;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 LQWACQ 7  
Db 31 LQWACQ 36

RESULT 15  
US-11-072-512-3534  
Sequence 3534, Application US/11072512  
Publication No. US2006029945A1

GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RIOTARO  
APPLICANT: TAMECHIKI, ICHIRO  
APPLICANT: SEKI, NAOHIKO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOTSUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084315-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2000-01-15  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 3534  
LENGTH: 800  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-072-512-3534

Query Match 11.8%; Score 6; DB 7; Length 800;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 QCSQNE 12  
Db 353 QCSQNE 358

Search completed: March 2, 2006, 04:42:39  
Job time : 22 SECs

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1	51	100.0	184	2	US-09-565-423-11	Sequence 1115, App
2	51	100.0	192	2	US-09-949-016-11115	Sequence 5, Appl
3	48	94.1	51	2	US-09-154-064-6	Sequence 6, Appl
4	48	94.1	181	2	US-09-854-064-5	Sequence 9, Appl
5	48	94.1	283	2	US-09-854-064-9	Sequence 21, Appl
6	44	87.3	58	2	US-09-154-064-21	Sequence 13, Appl
7	34	66.7	34	2	US-09-854-064-7	Sequence 12, Appl
8	34	66.7	81	2	US-09-854-064-13	Sequence 17, Appl
9	10	19.6	117	2	US-09-154-064-12	Sequence 11, Appl
10	10	19.6	185	2	US-09-565-423-17	Sequence 10, Appl
11	10	19.6	195	2	US-09-854-064-11	Sequence 1, Appl
12	10	19.6	281	2	US-09-154-064-10	Sequence 30, Appl
13	6	61.8	29	2	US-09-767-60339	Sequence 5704, Ap
14	6	11.8	62	2	US-09-621-976-5704	Sequence 2, Appl
15	6	11.8	74	2	US-09-110-052-2	Sequence 28241, A
16	6	11.8	80	2	US-09-248-796A-26829	Sequence 26829, A
17	6	11.8	110	2	US-09-248-796A-26879	Sequence 26879, A
18	6	11.8	111	2	US-09-710-767-44871	Sequence 44871, A
19	6	11.8	165	2	US-09-270-767-35026	Sequence 35026, A
20	6	11.8	165	2	US-09-270-767-50243	Sequence 50243, A
21	6	11.8	172	2	US-09-52-931A-28241	Sequence 28241, A
22	6	11.8	179	2	US-09-252-931A-22579	Sequence 25925, A
23	6	11.8	197	2	US-09-252-931A-22579	Sequence 23579, A
24	6	11.8	201	2	US-09-148-796A-19314	Sequence 19314, A
25	6	11.8	233	2	US-09-134-000C-5259	Sequence 5259, Ap
26	6	11.8	237	2	US-09-248-796A-14958	Sequence 14858, A
27	6	11.8	270	2	US-09-543-681A-4388	Sequence 4388, Ap

SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 11115  
 LENGTH: 192  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-11115

Query Match Best Local Similarity 100.0%; Score 51; DB 2; Length 192;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 US-09-854-864-6  
 Sequence 6, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-05-12  
 PRIOR APPLICATION NUMBER: US 60/214, 591  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6  
 LENGTH: 51  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-6

Query Match Best Local Similarity 100.0%; Score 48; DB 2; Length 51;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-09-854-864-5  
 Sequence 5, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-05-12  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-5

Query Match Best Local Similarity 94.1%; Score 48; DB 2; Length 181;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 US-09-854-864-9  
 Sequence 9, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-05-12  
 PRIOR APPLICATION NUMBER: US 60/214, 591  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 9  
 LENGTH: 283  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-9

Query Match Best Local Similarity 94.1%; Score 48; DB 2; Length 283;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 US-09-854-864-21  
 Sequence 21, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-05-12  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 21  
 LENGTH: 58  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-21

Query Match Best Local Similarity 86.3%; Score 44; DB 2; Length 58;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 US-09-854-864-51  
 Sequence 8, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-05-12  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-51

Query Match Best Local Similarity 100.0%; Score 44; DB 2; Length 58;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 US-09-854-864-44  
 Sequence 1, Application US/09854864  
 Patent No. 6774106  
 GENERAL INFORMATION:  
 APPLICANT: THEILL, LARS EYDE  
 ATTORNEY: YU, GANG  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
 FILE REFERENCE: A-686B  
 CURRENT APPLICATION NUMBER: US/09/854, 864  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: US 60/204, 039  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-854-864-44

**RESULT 7**  
US-09-854-864-7  
Sequence 7, Application US/09854864  
Patent No. 6774106  
GENERAL INFORMATION:  
APPLICANT: YU, GANG  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 7  
LENGTH: 34  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-864-7

Query Match 66.7%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.1e-29;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
US-09-854-864-13  
Sequence 13, Application US/09854864  
Db 1 CSQNEYFDSDLHACIPCOLRCSNTPPLTCORYC 41

**Qy** 8 CSQNEYFDSDLHACIPCOLRCSNTPPLTCORYC 41  
Db 1 CSQNEYFDSDLHACIPCOLRCSNTPPLTCORYC 34

GENERAL INFORMATION:  
Patent No. 6774106  
APPLICANT: YU, GANG  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 13  
LENGTH: 81  
TYPE: PRT  
ORGANISM: Consensus  
US-09-854-864-13

Query Match 66.7%; Score 34; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred. No. 8.6e-29;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 8 CSQNEYFDSDLHACIPCOLRCSNTPPLTCORYC 41  
Db 1 CSQNEYFDSDLHACIPCOLRCSNTPPLTCORYC 34

GENERAL INFORMATION:  
Patent No. 6774106  
APPLICANT: YU, GANG  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039

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; PRIORITY FILING DATE: 2000-05-12
; PRIORITY APPLICATION NUMBER: US 60/214,591
; PRIORITY FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match          11.8%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy   26 LRCSSN 31
Db   2 LRCSSN 7

RESULT 14
US-09-621-976-5704
; Sequence 5704, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET-054P42
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 5704
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SIGNAL
; NAME/KEY: SIGNAL
; LOCATION: -43.-1
US-09-621-976-5704

Query Match          11.8%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy   28 CSSNTP 33
Db   49 CSSNTP 54

RESULT 15
US-09-510-252-2
; Sequence 2, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: NDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US/09/510,252
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: US/09/510,252
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Any X can be any amino acid.
US-09-510-252-2

Query Match          11.8%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy   24 CQLRCS 29

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Db 44 CQLRCS 49

Search completed: March 2, 2006, 04:29:06  
Job time : 47 secs

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GenCore version 5.1.7  
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OM protein - protein search, using SW model

Run on: March 2, 2006, 04:20:42 ; Search time 235 Seconds  
(without alignment)  
153.115 Million cell updates/sec

Title: US-10-077-438-1\_COPY\_1\_51  
Perfect score: 51  
Sequence: 1 MLIQAGQCQNVEYFDLHLA.....TPPLTCQYCNASTNSVKG 51

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Gapop 60.0 , Gapext 60.0

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Word size: 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 05.80:  
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2: uniprot\_trembl:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	51	100.0	184	1 TNR17_HUMAN	Q02223 homo sapien
2	51	100.0	184	2 Q6PEA6_HUMAN	Q83e46 homo sapien
3	10	19.6	185	1 TNR17_MOUSE	Q83e72 mus musculus
4	8	15.7	148	2 Q5JK76_ORYSA	Q5jk16 oryza sativa
5	8	15.7	499	2 Q8B714_MOUSE	Q8B714 mus musculus
6	8	15.7	1674	2 Q8OZ18_MOUSE	Q8oZ18 mus musculus
7	8	15.7	2850	2 Q8OT03_MOUSE	Q8ot03 mus musculus
8	7	13.7	140	2 Q800M3_MORAM	Q800m3 morone amer
9	7	13.7	140	2 Q800M4_MORAM	Q800m4 morone chry
10	7	13.7	140	2 Q800M5_MORCS	Q800m5 morone saxa
11	7	13.7	140	2 Q800M6_MORSA	Q8blix4 mus musculus
12	7	13.7	175	2 Q8BHK4_MOUSE	Q9jdg3 human immun
13	7	13.7	202	2 Q9JDQ3_9HTY1	Q8lx76 chaoborus a
14	7	13.7	206	2 Q8LX76_9DIP7	Q8as74 human immun
15	7	13.7	207	2 Q8AS74_9HTIVI	Q8bhs1 mus musculus
16	7	13.7	258	2 Q8BBHS1_MOUSE	Q4yha8 plasmidium
17	7	13.7	264	2 Q4YHA8_PLABE	Q4yz16 plasmid
18	7	13.7	307	2 Q4YZ16_PLABE	Q5dib6 epinephelus
19	7	13.7	307	2 Q5DIB6_EPICO	Q9wyx9_themba
20	7	13.7	309	2 Q9WYX9_THEME	Q9wyx9 thermotoga
21	7	13.7	333	2 Q678F3_9VIRU	Q678f3 lymphocysti
22	7	13.7	385	2 Q6MT77_MYCMS	Q6mt77 mycoplasma
23	7	13.7	409	2 Q67205_9HTIVI	Q67205 human immun
24	7	13.7	411	2 Q5FW06_XENTR	Q5fw06 xenopus tro
25	7	13.7	412	2 Q5U4G6_MOUSE	Q5u4g6 mus musculus
26	7	13.7	412	2 Q8K3A5_MOUSE	Q8k3a5 mus musculus
27	7	13.7	412	2 QBBHQ2_MOUSE	Qbbhq2 mus musculus
28	7	13.7	413	2 Q4HZP5_GIBZE	Q4hzp5 gibberella
29	7	13.7	457	2 Q8AVS9_XENLA	Q8av9 xenopus lae
30	7	13.7	804	2 QBWRL8_TETTH	Q8wrl8 terraymena
31	7	13.7	945	2 Q52FS8_MAGGR	Q52fs8 magnaporthe

## Best Available Copy

RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; "NIEHS-SNPs, environmental genome project, NIEHS ES15478; Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu/>)."; RT Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

[6] RN FUNCTION, AND INTERACTIONS WITH TRAF1, AND TRAF3.  
RX MEDLINE=20363816; PubMed=1903733;  
RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J.-I., Devergne O., Tsapis A.; "B cell maturation associates with TNF receptor family member BCMA (B cell maturation factor (TRAF) 1, TRAF2, and TRAF3 and activates NF- $\kappa$ B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-activated protein kinase"; Immunol. 165:1322-1330 (2000)."  
RN FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.  
RX MEDLINE=21170294; PubMed=1097384; DOI=10.1038/35010115;  
RA Yu G., Boone T., Johnstone J., Mudri S., Enseiman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harren K., Kindzogel W., Clegg C.H.; "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell autoimmune disease"; Nature 404:995-999 (2000).  
RN RP INTERACTIONS WITH APRIL AND TRAF6.  
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
RA Shu H.-B., Johnson H.; "B cell maturation protein is a receptor for the tumor necrosis factor family member TALL-1"; Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161 (2000).  
CC -!- FUNCTION: Receptor for TNF $\alpha$ /13B/lys/BAFF and TNFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF- $\kappa$ B and JNK.  
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC -!- INTERACTION: Q9Y275; NbExp=1; IntAct=EBI-519945; EBI-519169;  
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.  
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-cells or monocytes.  
CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation t(4;16)(Q26;P13) with IL2.  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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CC EMBL: 214954; CAM78679.1; mRNA.  
DR EMBL: 229575; CARB2691.1; mRNA.  
DR EMBL: 229574; CARB2690.1; Genomic DNA.  
DR EMBL: U95742; AAEB7251.1; Genomic DNA.  
DR EMBL: U95772; AB60895.1; Genomic DNA.  
DR EMBL: AY509112; ARAB8240.1; Genomic DNA.  
DR PIR: S43486.  
DR PDB: 1XU2; X-ray; R/S/T=5-51.  
DR IntAct: Q02223; Homo sapiens.  
DR Ensembl: ENSG0000048462; Homo sapiens.  
DR HGNC: HGNC:11913; TNFRSF17.

RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; "NIEHS-SNPs, environmental genome project, NIEHS ES15478; Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu/>)."; RT Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

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RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J.-I., Devergne O., Tsapis A.; "B cell maturation associates with TNF receptor family member BCMA (B cell maturation factor (TRAF) 1, TRAF2, and TRAF3 and activates NF- $\kappa$ B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-activated protein kinase"; Immunol. 165:1322-1330 (2000)."  
RN FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.  
RX MEDLINE=21170294; PubMed=1097384; DOI=10.1038/35010115;  
RA Yu G., Boone T., Johnstone J., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Hawkin N., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theilig L.E.; "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating humoral immunity"; Nat. Immunol. 1:252-256 (2000).  
RN RP INTERACTIONS WITH APRIL AND TRAF6.  
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
RA Shu H.-B., Johnson H.; "B cell maturation protein is a receptor for the tumor necrosis factor family member TALL-1"; Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161 (2000).  
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CC -!- INTERACTION: Q9Y275; NbExp=1; IntAct=EBI-519945; EBI-519169;  
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.  
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-cells or monocytes.  
CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation t(4;16)(Q26;P13) with IL2.  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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DR EMBL: U95742; AAEB7251.1; Genomic DNA.  
DR EMBL: U95772; AB60895.1; Genomic DNA.  
DR EMBL: AY509112; ARAB8240.1; Genomic DNA.  
DR PIR: S43486.  
DR PDB: 1XU2; X-ray; R/S/T=5-51.  
DR IntAct: Q02223; Homo sapiens.  
DR Ensembl: ENSG0000048462; Homo sapiens.  
DR HGNC: HGNC:11913; TNFRSF17.





NUCLEOTIDE SEQUENCE									
SQ	SEQUENCE	1674 AA;	181168 MW;	3BC42CB004476309 CRC64;	RA	Fruchtmann S., Hawkins M.B., Borski R.J.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
	Query Match	15.7%;	Score 8;	DB 2;	Length 1674;	RL	-1 - FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).		
	Best Local Similarity	100.0%;	Pred. No. 15;			CC	-1 - SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).		
	Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	CC	CC		
Qy	8 CSQNEYFD 15					CC	CC		
Db	1181 CSQNEYFD 1188					CC	CC		
RESULT 7									
QB0T03	MOUSE PRELIMINARY;	PRT;	2850 AA.			DR	HSSP; AF402676; AA073861.1; - ; mRNA.		
ID	QB0T03_MOUSE					DR	HSRP; P080659; 1JOH.		
AC	QB0T03;					DR	SMR; Q80003; 1-140.		
DT	01-JUN-2003 (TREMBLrel. 24, Created)					DR	GO; GO:000524; F:ATP binding; IEA.		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)					DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					DR	GO; GO:0004872; F:receptor activity; IEA.		
DE	MUC6.					DR	GO; GO:0016740; F:transferase activity; IEA.		
GN	Name=Muc6;					DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
OS	Mus musculus (Mouse)					DR	InterPro; IPR001245; Tyr_Pkinase_AS.		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;					DR	InterPro; IPR008266; Tyr_Pkinase_AS.		
NCBI_TaxID	10090;					DR	PRINTS; PRO000109; TYRKINASE.		
RN						DR	ProdDom; PD000001; Prot_kinase_1.		
RP						DR	DRUGB; PS50011; PROTEIN_KINASE_DOM; 1.		
RC	STRAIN=57BL/6J;					DR	PROSITE; PS00105; PROTEIN_KINASE_TYR; 1.		
RX	MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;					KW	Receptor.		
RA	Desseyn J.-L., Laine A.;					PT	NON_TER 1 140 140		
RT	"Characterization of mouse muc6 and evidence of conservation of the gel-forming mucin gene cluster between human and mouse.";					PT	NON_TER 1 140 140		
RT	Genomics 81:433-436 (2003).					PT	NON_TER 1 140 140		
RL	DR					SEQUENCE	140 AA; 15787 MW; BB1B2C98A17B541B CRC64;		
EMBL	AV184388; AA047735.1; -; Genomic DNA.					Query	1 MLQMAGQ 7		
EMBL	AV184385; AA047735.1; JOINED; Genomic DNA.					DR	1 103 MLQMAGQ 109		
EMBL	AV184387; AA047735.1; JOINED; Genomic DNA.								
EMBL	AV184386; AA047735.1; JOINED; Genomic DNA.								
HSSP	OG6162; 1KJ0								
DR	Ensembl: ENSEMBL0000048191; Mus musculus.								
MGI	MGI: 2663233; Muc6.								
DR	InterPro; IPR006207; Cys_knot_C.								
DR	InterPro; IPR02941; Prot_Inh_CR_TIL.								
DR	InterPro; IPR001846; VWF_D.								
DR	PFam; PF01826; TIL; 2.								
DR	SMART; SM00216; VWD; 3.								
DR	PROSITE; PS01225; CTCK_2; 1.								
SEQUENCE	2850 AA; 300398 MW; 9CD95F0845CT9C9D CRC64;								
Qy	8 CSQNEYFD 15								
Db	* 1222 CSQNEYFD 1229								
RESULT 8									
QB00M3	MORAM PRELIMINARY;	PRT;	140 AA.			RP	NUCLEOTIDE SEQUENCE.		
ID	QB00M3_MORAM					RA	Fruchtmann S., Hawkins M.B., Borski R.J.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
AC	QB00M3;					RL	-1 - FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).		
DT	01-JUN-2003 (TREMBLrel. 24, Created)					CC	-1 - SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)					CC	CC		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					CC	CC		
DE	Insluin-like growth factor I receptor (Fragment).					CC	CC		
OS	Morone americana (White perch).					CC	CC		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleosteoi; Osteoleosteoi; Acanthomorphia; Acanthopterygii; Perciformes; Percoidae; Moronidae; Morone.					CC	CC		
NCBI_TaxID	46260;					CC	CC		
RN	[1]					CC	CC		
RESULT 9									
QB00M4	MORCH PRELIMINARY;	PRT;	140 AA.			RP	NUCLEOTIDE SEQUENCE.		
ID	QB00M4_MORCH					RA	Fruchtmann S., Hawkins M.B., Borski R.J.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
AC	QB00M4;					RL	-1 - FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)					CC	-1 - SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature oocytes (By similarity).		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					CC	CC		
DE	Insluin-like growth factor I receptor (Fragment).					CC	CC		
OS	Morone americana (White perch).					CC	CC		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleosteoi; Osteoleosteoi; Acanthomorphia; Acanthopterygii; Perciformes; Percoidae; Moronidae; Morone.					CC	CC		
NCBI_TaxID	46260;					CC	CC		
RN	[1]					CC	CC		



RC	STRAIN=CS7BL/6J; TISSUE=Head;	RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RA	Carninci P., Hayashizaki Y.;	DR	EMBL; AK076417; BAC16330.1; - ; mRNA.
RT	"High-efficiency full-length cDNA cloning.";	DR	Ensembl; ENSMUSG00000035572; Mus musculus.
RL	Meth. Enzymol. 303:19-44 (1999).	DR	MGI; MGI:2140179; AA599934.
RN	[2]	DR	MGI; MGI:2140179; WD32.
RP	NUCLEOTIDE SEQUENCE.	DR	InterPro; IPR001680; WD40.
RC	STRAIN=CS7BL/6J; TISSUE=Head;	DR	PFam; PF00400; WD40; 1.
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	DR	SMART; SM00320; WD40; 1.
RA	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,	KW	Hypothetical protein.
RA	Aizawa T., Hara A., Furukoshi Y., Konno H., Adachi J., Kiyosawa H.,	FT	FT
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,	SEQUENCE	175 AA; 19571 MW; D5A62B8785D9F10F CRC64;
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	Query	Match 13.7%; Score 7; DB 2;
RA	Kadota K., Matsuda H.A., Ashburner B., Batalov S., Casavant T.,	Best Local Similarity 100.0%; Pred. No. 25;	Length 175;
RA	Pleischmann W., Gaasterland T., Gissi C., King B., Koschwa H.,	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pelle G., Quackenbush J.,	Qy	26 LRCSSNT 32
RA	Schrimal L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	Db	43 LRCSSNT 49
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brooks-Wilson A.M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,		
RA	Gustincich S., Hill D., Hotzmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarrelli J., Mombaerts P.,		
RA	Nordheim P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-P.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshiida K., Hasegawa Y., Kawaji H., Kohetsuki S.,		
RA	Hayashizaki Y.,		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RN	Nature 409:685-690 (2000).		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	The PHANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573 (2002).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Shibata K., Itoh M., Aizawa K., Nagachika S., Sasaki N., Carninci P.,		
RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,		
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishina T., Harada A.,		
RA	Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,		
RA	Fujikake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachiki M.,		
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,		
RA	Oka Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,		
RT	"RIKEN integrated sequence analysis (RISA) system-384 format		
RT	sequencing pipeline with 384 multicapillary sequencer.";		
RL	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RX	MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagachika S., Sasaki N., Carninci P.,		
RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
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RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
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RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
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RA	Aizawa T., Hara A., Furukoshi Y., Konno H., Adachi J., Kiyosawa H.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner B., Batalov S., Casavant T.,		
RA	Pleischmann W., Gaasterland T., Gissi C., King B., Koschwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pelle G., Quackenbush J.,		
RA	Schrimal L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brooks-Wilson A.M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,		
RA	Gustincich S., Hill D., Hotzmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Nordheim P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-P.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshiida K., Hasegawa Y., Kawaji H., Kohetsuki S.,		
RA	Hayashizaki Y.,		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RN	Nature 409:685-690 (2000).		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RA	Shibata K., Aizawa K., Sugahara Y., Shibata K., Itoh M.,		
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,		
RA	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RT	Genome Res. 10:1617-1630 (2000);		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RX	MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagachika S., Sasaki N., Carninci P.,		
RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,		
RA	Fujikake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachiki M.,		
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,		
RA	Oka Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,		
RT	"RIKEN integrated sequence analysis (RISA) system-384 format		
RT	sequencing pipeline with 384 multicapillary sequencer.";		
RL	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Kawai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Kawai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Kawai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,		
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
RA	Nishi K., Nomura K., Numasaki R., Ono M., Ohzato N., Okazaki Y.,		
RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
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RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
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RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagewa I., Kasukawa T.,		
RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
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RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
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RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Kawai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
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RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
RN	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CS7BL/6J; TISSUE=Head;		
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RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
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RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
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RT	Genome Res. 10:1757-1771 (2000).		
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RA	Katoh H., Kawai J., Koijima Y., Kondo H., Konno H., Kouda M., Koya S.,		
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,		
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RA	Saito R., Saitoh H., Sakai C., Sano H., Saito K., Shiraki T., Tagami M.,		
RA	Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Tagami Y., Takeda Y.,		
RA	Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,		
RT	Genome Res. 10:1757-1771 (2000).		
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RC	STRAIN=CS7BL/6J; TISSUE=Head;		
RA	Kawai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T		

OS Chaoborus americanus.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Culicoidae; Chaoboridae;  
 OC Chaoborus.  
 OX NCBI\_TaxID=204565;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Berendsen T.U.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ427818; CAD44504.1; -; Genomic DNA.  
 DR GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ 206 AA; 23927 MW; E6BC8651EABA571 CRC64;

Query Match 13.7%; Score 7; DB 2; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 29 SSNTPPL 35  
 Db 137 SSNTPPL 143

RESULT 15  
 ID QAS74\_9HTV1  
 ID QAS74\_9HTV1 PRELIMINARY;  
 AC  
 DR 01-MAR-2003 (TREMBLrel. 23; Created)  
 DR 01-JUN-2003 (TREMBLrel. 23; Last sequence update)  
 DR 01-JUN-2003 (TREMBLrel. 24; Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Wang Y.; Frey S.; Gupta P.; Learn G.H.; Mittler J.; Shriner D.;  
 RA Nickle D.C.; Jensen M.A.; Rodrigo A.G.; He X.; Zhao H.;  
 RA Rossini A.; Felsenstein J.; Walker B.D.; Mullins J.I.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF535413; AAN07372.1; -; Genomic\_C\_RNA.  
 DR SNR; QAS74\_1-207.  
 DR GO:GO:0016021; C:integral to membrane; IEA.  
 DR GO:GO:19031; C:civil envelope; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Envelope protein; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 207 207  
 SQ 2946 MW; DCD2182D0A73F90B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 25 QLRCSNN 31  
 Db 174 QLRCSNN 180